

## SEQUENCE LISTING

<110> McGill University  
 Herscovics, Annette A.  
 Tremblay, Linda O.

<120> ALPHA 1,2-MANNOSIDASE AND THERAPEUTICAL  
 USES THEREOF

<130> 1770-228PCT

<140> PCT/CA/00/00775  
 <141> 2000-06-28

<150> US 60/140,992  
 <151> 1999-06-29

<160> 19

<170> FastSEQ for windows Version 3.0

<210> 1  
 <211> 21  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> sense primer

<400> 1  
 ccacagacc agcaaggtgc c 21

<210> 2  
 <211> 21  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Antisense primer

<400> 2  
 ctaggcaggg gtccagatag g 21

<210> 3  
 <211> 23  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> GSP1 primer

<400> 3  
 gggcacttct gctcttcttg aag 23

<210> 4  
 <211> 22  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> GSP2 sense primer

<400> 4  
 atgactgtcc tctgcgatc tc 22

<210> 5  
 <211> 21  
 <212> DNA

## 52310-seq listing

<213> Artificial Sequence  
 <220>  
 <223> GSP3.1 antisense primer  
 <400> 5  
 tgtcttctgt gacgaaatct c 21  
 <210> 6  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> GSP3.2 sense primer  
 <400> 6  
 cagagctttc caatggtcag c 21  
 <210> 7  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> GSP3.3 antisense primer  
 <400> 7  
 tcatagctct cgccaaagct cagc 24  
 <210> 8  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Sense primer  
 <400> 8  
 atcgggactt cacctcggtg 20  
 <210> 9  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Sense primer  
 <221> misc\_feature  
 <222> (4)...(9)  
 <223> EcoRI site  
 <400> 9  
 aaagaattcc agattagacc cccaagccaa g 31  
 <210> 10  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense primer SHMSTOP  
 <221> misc\_feature  
 <222> (4)...(9)  
 <223> XbaI site

# 52310-seq listing

<400> 10  
 aaatctagac taggcagggg tccagatagg 30  
 <210> 11  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Sense primer  
 <221> misc\_feature  
 <222> (4)...(9)  
 <223> EcoRI site  
 <400> 11  
 aaagaattcc agggcacacc agtgcattctg 30  
 <210> 12  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense primerSHMR  
 <221> misc\_feature  
 <222> (4)...(9)  
 <223> XbaI site  
 <400> 12  
 aaatctagag caggggtcca gataggcag 29  
 <210> 13  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Sense primer for producing R461L  
 <400> 13  
 gtattcacgc tgggcgcttt ggccgacagc tactatg 37  
 <210> 14  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Antisense primer for producing R461L  
 <400> 14  
 catagtagct gtcggccaaa gcgcccagcg tgaatac 37  
 <210> 15  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Sense primer  
 <221> misc\_feature  
 <222> (5)...(10)  
 <223> Hind III  
 <400> 15

## 52310-seq listing

aaaaaagctt ccaccatggc tgcctgcgag ggcaggag	38
<210> 16	
<211> 41	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Antisense primer	
<221> misc_feature	
<222> (9)...(16)	
<223> Not 1 site	
<400> 16	
aaaaaaaagc ggccgctagg caggggtcca gataggcaga g	41
<210> 17	
<211> 41	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> antisense primer containing a Not 1 site	
<221> misc_feature	
<222> (9)...(16)	
<223> Not 1 site	
<400> 17	
aaaaaaaagc ggccgcgagg caggggtcca gataggcaga g	41
<210> 18	
<211> 2739	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Human alpha1,2-mannosidase cDNA	
<221> CDS	
<222> (51)...(2147)	
<223> Human alpha1,2-mannosidase	
<400> 18	
cgcacgcgca gtcgtatccg tgtgatgggc gggctgttga cggcgctgcg atg gct	56
	Met Ala
	1
gcc tgc gag ggc agg aga agc gga gct ctc ggt tcc tct cag tcg gac	104
Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser Gln Ser Asp	
5 10 15	
ttc ctg acg ccg cca gtg ggc ggg gcc cct tgg gcc gtc gcc acc act	152
Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala Val Ala Thr Thr	
20 25 30	
gta gtc atg tac cca ccg ccg ccg ccg ccg cct cat cgg gac ttc atc	200
Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro His Arg Asp Phe Ile	
35 40 45 50	
tcg gtg acg ctg agc ttt ggc gag agc tat gac aac agc aag agt tgg	248
Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr Asp Asn Ser Lys Ser Trp	
55 60 65	
cgg cgg cgc tcg tgc tgg agg aaa tgg aag caa ctg tcg aga ttg cag	296
Arg Arg Arg Ser Cys Trp Arg Lys Trp Lys Gln Leu Ser Arg Leu Gln	
70 75 80	

## 52310-seq listing

cgg	aat	atg	att	ctc	ttc	ctc	ctt	gcc	ttt	ctg	ctt	ttc	tgt	gga	ctc	344
Arg	Asn	Met	Ile	Leu	Phe	Leu	Leu	Ala	Phe	Leu	Leu	Phe	Cys	Gly	Leu	
		85					90					95				
ctc	ttc	tac	atc	aac	ttg	gct	gac	cat	tgg	aaa	gct	ctg	gct	ttc	agg	392
Leu	Phe	Tyr	Ile	Asn	Leu	Ala	Asp	His	Trp	Lys	Ala	Leu	Ala	Phe	Arg	
	100					105					110					
cta	gag	gaa	gag	cag	aag	atg	agg	cca	gaa	att	gct	ggg	tta	aaa	cca	440
Leu	Glu	Glu	Glu	Gln	Lys	Met	Arg	Pro	Glu	Ile	Ala	Gly	Leu	Lys	Pro	
	115				120					125					130	
gca	aat	cca	ccc	gtc	tta	cca	gct	cct	cag	aag	gcg	gac	acc	gac	cct	488
Ala	Asn	Pro	Pro	Val	Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr	Asp	Pro	
				135					140					145		
gag	aac	tta	cct	gag	att	tcg	tca	cag	aag	aca	caa	aga	cac	atc	cag	536
Glu	Asn	Leu	Pro	Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	
			150					155					160			
cgg	gga	cca	cct	cac	ctg	cag	att	aga	ccc	cca	agc	caa	gac	ctg	aag	584
Arg	Gly	Pro	Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp	Leu	Lys	
		165					170					175				
gat	ggg	acc	cag	gag	gag	gcc	aca	aaa	agg	caa	gaa	gcc	cct	gtg	gat	632
Asp	Gly	Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	
	180					185					190					
ccc	cgc	ccg	gaa	gga	gat	ccg	cag	agg	aca	gtc	atc	agc	tgg	agg	gga	680
Pro	Arg	Pro	Glu	Gly	Asp	Pro	Gln	Arg	Thr	Val	Ile	Ser	Trp	Arg	Gly	
	195				200					205					210	
gcg	gtg	atc	gag	cct	gag	cag	ggc	acc	gag	ctc	cct	tca	aga	aga	gca	728
Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg	Ala	
				215					220					225		
gaa	gtg	ccc	acc	aag	cct	ccc	ctg	cca	ccg	gcc	agg	aca	cag	ggc	aca	776
Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln	Gly	Thr	
			230					235					240			
cca	gtg	cat	ctg	aac	tat	cgc	cag	aag	ggc	gtg	att	gac	gtc	ttc	ctg	824
Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp	Val	Phe	Leu	
		245					250					255				
cat	gca	tgg	aaa	gga	tac	cgc	aag	ttt	gca	tgg	ggc	cat	gac	gag	ctg	872
His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly	His	Asp	Glu	Leu	
	260					265					270					
aag	cct	gtg	tcc	agg	tcc	ttc	agt	gag	tgg	ttt	ggc	ctc	ggg	ctc	aca	920
Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe	Gly	Leu	Gly	Leu	Thr	
	275				280					285					290	
ctg	atc	gac	gcg	ctg	gac	acc	atg	tgg	atc	ttg	ggg	ctg	agg	aaa	gaa	968
Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile	Leu	Gly	Leu	Arg	Lys	Glu	
				295					300					305		
ttt	gag	gaa	gcc	agg	aag	tgg	gtg	tcg	aag	aag	tta	cac	ttt	gaa	aag	1016
Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser	Lys	Lys	Leu	His	Phe	Glu	Lys	
			310					315					320			
gac	gtg	gac	gtc	aac	ctg	ttt	gag	agc	acg	atc	cgc	atc	ctg	ggg	ggg	1064
Asp	Val	Asp	Val	Asn	Leu	Phe	Glu	Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	
		325					330					335				
ctc	ctg	agt	gcc	tac	cac	ctg	tct	ggg	gac	agc	ctc	ttc	ctg	agg	aaa	1112
Leu	Leu	Ser	Ala	Tyr	His	Leu	Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	

## 52310-seq listing

340	345	350	
gct Ala 355	gag Glu	gat Asp	ttt Phe
gga Gly	aat Asn 360	cgg Arg	cta Leu
atg Met	cct Pro	gcc Ala 365	ttc Phe
aga Arg	aca Thr	cca Pro	tcc Ser 370
1160			
aag Lys	att Ile	cct Pro	tac Tyr
tcg Ser 375	gat Asp	gtg Val	aac Asn
atc Ile	ggt Gly 380	act Thr	gga Gly
ggt Val	gcc Ala	cac His 385	ccg Pro
1208			
cca Pro	cgg Arg	tgg Trp	acc Thr 390
tcc Ser	gac Asp	agc Ser	act Thr
gtg Val 395	gcc Ala	gag Glu	gtg Val
acc Thr	agc Ser 400	att Ile	cag Gln
1256			
ctg Leu	gag Glu	ttc Phe 405	cgg Arg
gag Glu	ctc Leu	tcc Ser	cgt Arg 410
ctc Leu	aca Thr	ggg Gly	gat Asp
aag Lys 415	aag Lys	ttt Phe	cag Gln
1304			
gag Glu	gca Ala 420	gtg Val	gag Glu
aag Lys	gtg Val	aca Thr 425	cag Gln
cac His	atc Ile	cac His	ggc Gly 430
ctg Leu	tct Ser	ggg Gly	aag Lys
1352			
aag Lys 435	gat Asp	ggg Gly	ctg Leu
gtg Val	ccc Pro 440	atg Met	ttc Phe
atc Ile	aat Asn	acc Thr 445	cac His
agt Ser	ggc Gly	ctc Leu	ttc Phe 450
1400			
acc Thr	cac His	ctg Leu	ggc Gly 455
gta Val 455	ttc Phe	acg Thr	ctg Leu
ggc Gly	gcc Ala 460	agg Arg	gcc Ala
gac Asp	agc Ser	tac Tyr 465	tat Tyr
1448			
gag Glu	tac Tyr	ctg Leu	ctg Leu
aag Lys	cag Gln	tgg Trp	atc Ile
cag Gln 475	ggc Gly	ggg Gly	aag Lys
cag Gln	gag Glu	aca Thr 480	cag Gln
1496			
ctg Leu	ctg Leu	gaa Glu 485	gac Asp
tac Tyr	gtg Val	gaa Glu 490	atc Ile
gag Glu	ggt Gly	gtc Val	aga Arg 495
acg Thr	cac His	ctg Leu	gcc Ala
1544			
ctg Leu	cgg Arg 500	cac His	tcc Ser
gag Glu	ccc Pro 505	agt Ser 505	aag Lys
ctc Leu	acc Thr	ttt Phe	gtg Val 510
ggg Gly	gag Glu	ggg Gly	gag Glu
ctt Leu	gcc Ala	cca Pro 530	cca Pro 530
1592			
cac His 515	ggc Gly	cgc Arg	ttc Phe
agt Ser	gcc Ala 520	aag Lys	atg Met
gac Asp	cac His	ctg Leu 525	gtg Val
tgc Cys	ttc Phe	ctg Leu	cca Pro 530
1640			
ggg Gly	acg Thr	ctg Leu	gct Ala
ctg Leu	ggc Gly	gtc Val	gtc Val
tac Tyr	cac His	ggc Gly 540	ctg Leu
ccc Pro	gcc Ala	agc Ser	cac His 545
atg Met			
1688			
gag Glu	ctg Leu	gcc Ala 550	cag Gln
gtg Val	atg Met	gag Glu	act Thr 555
tgt Cys	tac Tyr	cag Gln	atg Met
aac Asn 560	cgg Arg	cag Gln	
1736			
atg Met	gag Glu	acg Thr 565	ggg Gly
ctg Leu	agt Ser	ccc Pro	gag Glu
atc Ile	gtg Val	cac His	ttc Phe
aac Asn 575	ctt Leu	tac Tyr	ccc Pro
1784			
cag Gln	ccg Pro 580	ggc Gly	cgt Arg
cgg Arg	gac Asp	gtg Val 585	gag Glu
gtc Val	aag Lys	cca Pro	gca Ala 590
gac Asp	agg Arg	cac His	aac Asn
1832			
ctg Leu	ctg Leu	cgg Arg	cca Pro
gag Glu	acc Thr	gtg Val	gag Glu
agc Ser	ctg Leu	agg Arg	ctg Leu
ctg Leu	tac Tyr	cgc Arg	gtc Val
1880			

## 52310-seq listing

595	600	605	610	
aca ggg gac cgc aaa tac cag gac tgg ggc tgg gag att ctg cag agc				1928
Thr Gly Asp Arg Lys 615	Tyr Gln Asp Trp Gly 620	Trp Glu Ile Leu Gln 625	Ser	
ttc agc cga ttc aca cgg gtc ccc tcg ggt ggc tat tct tcc atc aac				1976
Phe Ser Arg Phe 630	Thr Arg Val Pro Ser 635	Gly Gly Tyr Ser Ser 640	Ile Asn	
aat gtc cag gat cct cag aag ccc gag cct agg gac aag atg gag agc				2024
Asn Val Gln 645	Pro Gln Lys Pro 650	Glu Pro Arg Asp Lys 655	Met Glu Ser	
ttc ttc ctg ggg gag acg ctc aag tat ctg ttc ttg ctc ttc tcc gat				2072
Phe Phe 660	Leu Gly Glu Thr Leu Lys Tyr Leu Phe 665	Leu Leu Phe Ser	Asp	
gac cca aac ctg ctc agc ctg gac gcc tac gtg ttc aac acc gaa gcc				2120
Asp Pro Asn Leu Leu Ser 680	Leu Asp Ala Tyr Val 685	Phe Asn Thr Glu Ala 690		
cac cct ctg cct atc tgg acc cct gcc taggggtggat ggctgctggt				2167
His Pro Leu Pro Ile 695	Trp Thr Pro Ala			
gtggggactt cgggtgggca gaggcacctt gctgggtctg tggcattttc caaggccac				2227
gtagcaccgg caaccgccaa gtggcccagg ctctgaactg gctctgggct cctcctcgtc				2287
tctgctttaa tcaggacacc gtgaggacaa gtgaggccgt cagtcttggt gtgatgcggg				2347
gtgggctggg ccgctggagc ctccgcctgc ttcctccaga agacacgaat catgactcac				2407
gattgctgaa gcctgagcag gtctctgtgg gccgaccaga ggggggcttc gaggtgggtcc				2467
ctgggtactgg ggtgaccgag tggacagccc aggggtgcagc tctgcccggg ctctgtgaagc				2527
ctcagrtgtc cccaatccaa gggctctggag gggctgcccgt gactccagag gcctgaggct				2587
ccagggctgg ctctgggtgt tacaagctgg actcagggat cctcctggcc gcccgcagg				2647
gggcttgagg ggctggacgg caagtccgtc tagctcacgg gcccctccag tggaatgggt				2707
cttttcgggtg gagataaaag ttgatttgct ct				2739

&lt;210&gt; 19

&lt;211&gt; 699

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Peptide

&lt;400&gt; 19

Met	Ala	Ala	Cys	Glu	Gly	Arg	Arg	Ser	Gly	Ala	Leu	Gly	Ser	Ser	Gln
1				5					10					15	
Ser	Asp	Phe	Leu	Thr	Pro	Pro	Val	Gly	Gly	Ala	Pro	Trp	Ala	Val	Ala
			20					25					30		
Thr	Thr	Val	Val	Met	Tyr	Pro	Pro	Pro	Pro	Pro	Pro	Pro	His	Arg	Asp
		35					40					45			
Phe	Ile	Ser	Val	Thr	Leu	Ser	Phe	Gly	Glu	Ser	Tyr	Asp	Asn	Ser	Lys
		50				55					60				
Ser	Trp	Arg	Arg	Arg	Ser	Cys	Trp	Arg	Lys	Trp	Lys	Gln	Leu	Ser	Arg
					70				75						80
Leu	Gln	Arg	Asn	Met	Ile	Leu	Phe	Leu	Leu	Ala	Phe	Leu	Leu	Phe	Cys
			85					90						95	
Gly	Leu	Leu	Phe	Tyr	Ile	Asn	Leu	Ala	Asp	His	Trp	Lys	Ala	Leu	Ala
			100					105					110		
Phe	Arg	Leu	Glu	Glu	Gln	Lys	Met	Arg	Pro	Glu	Ile	Ala	Gly	Leu	
		115				120					125				
Lys	Pro	Ala	Asn	Pro	Pro	Val	Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr
		130				135					140				
Asp	Pro	Glu	Asn	Leu	Pro	Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His
				150						155					160
Ile	Gln	Arg	Gly	Pro	Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp

## 52310-seq listing

Leu	Lys	Asp	Gly	Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro
			180	165				170					175		
Val	Asp	Pro	Arg	Pro	Glu	Gly	Asp	185	Pro	Gln	Arg	Thr	Val	Ile	Ser
		195					200						205		Trp
Arg	Gly	Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg
	210				215					220					
Arg	Ala	Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln
225					230					235					240
Gly	Thr	Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp	Val
				245					250					255	
Phe	Leu	His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly	His	Asp
			260					265					270		
Glu	Leu	Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe	Gly	Leu	Gly
		275					280					285			
Leu	Thr	Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile	Leu	Gly	Leu	Arg
	290					295					300				
Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser	Lys	Lys	Leu	His	Phe
305					310					315					320
Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu	Ser	Thr	Ile	Arg	Ile	Leu
				325					330					335	
Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu	Ser	Gly	Asp	Ser	Leu	Phe	Leu
			340					345					350		
Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn	Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr
		355					360					365			
Pro	Ser	Lys	Ile	Pro	Tyr	Ser	Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala
	370					375					380				
His	Pro	Pro	Arg	Trp	Thr	Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser
385					390					395					400
Ile	Gln	Leu	Glu	Phe	Arg	Glu	Leu	Ser	Arg	Leu	Thr	Gly	Asp	Lys	Lys
				405					410					415	
Phe	Gln	Glu	Ala	Val	Glu	Lys	Val	Thr	Gln	His	Ile	His	Gly	Leu	Ser
			420					425					430		
Gly	Lys	Lys	Asp	Gly	Leu	Val	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly
		435					440					445			
Leu	Phe	Thr	His	Leu	Gly	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser
	450				455						460				
Tyr	Tyr	Glu	Tyr	Leu	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu
465					470					475					480
Thr	Gln	Leu	Leu	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg	Thr
				485					490					495	
His	Leu	Leu	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val	Gly	Glu
			500					505					510		
Leu	Ala	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu	Val	Cys	Phe
		515					520					525			
Leu	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly	Leu	Pro	Ala	Ser
	530					535					540				
His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr	Cys	Tyr	Gln	Met	Asn
545					550					555					560
Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu	Ile	Val	His	Phe	Asn	Leu
				565					570					575	
Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val	Glu	Val	Lys	Pro	Ala	Asp	Arg
			580					585					590		
His	Asn	Leu	Leu	Arg	Pro	Glu	Thr	Val	Glu	Ser	Leu	Phe	Tyr	Leu	Tyr
		595					600					605			
Arg	Val	Thr	Gly	Asp	Arg	Lys	Tyr	Gln	Asp	Trp	Gly	Trp	Glu	Ile	Leu
	610					615					620				
Gln	Ser	Phe	Ser	Arg	Phe	Thr	Arg	Val	Pro	Ser	Gly	Gly	Tyr	Ser	Ser
625					630					635					640
Ile	Asn	Asn	Val	Gln	Asp	Pro	Gln	Lys	Pro	Glu	Pro	Arg	Asp	Lys	Met
				645					650					655	
Glu	Ser	Phe	Phe	Leu	Gly	Glu	Thr	Leu	Lys	Tyr	Leu	Phe	Leu	Leu	Phe
			660					665					670		
Ser	Asp	Asp	Pro	Asn	Leu	Leu	Ser	Leu	Asp	Ala	Tyr	Val	Phe	Asn	Thr
		675					680					685			
Glu	Ala	His	Pro	Leu	Pro	Ile	Trp	Thr	Pro	Ala					
	690					695									